# Final Progress Report for Research Projects Funded by Health Research Grants

Instructions: Please complete all of the items as instructed. Do not delete instructions. Do not leave any items blank; responses must be provided for all items. If your response to an item is "None", please specify "None" as your response. "Not applicable" is not an acceptable response for any of the items. There is no limit to the length of your response to any question. Responses should be single-spaced, no smaller than 12-point type. The report **must be completed using MS Word**. Submitted reports must be Word documents; they should not be converted to pdf format. Questions? Contact Health Research Program staff at 717-783-2548.

- 1. Grantee Institution: Children's Hospital of Pittsburgh of the UPMC Health System
- 2. Reporting Period (start and end date of grant award period): 1/1/11 to 12/31/13
- 3. Grant Contact Person (First Name, M.I., Last Name, Degrees): David H. Perlmutter, MD
- 4. Grant Contact Person's Telephone Number: (412) 692-6081
- 5. Grant SAP Number: 4100054844
- 6. **Project Number and Title of Research Project:** Project #1 Regulation of Aging by the Proteasomal Pathway
- 7. Start and End Date of Research Project: 1/1/11 to 12/31/13
- 8. Name of Principal Investigator for the Research Project: Arjumand Ghazi, PhD
- 9. Research Project Expenses.
  - 9(A) Please provide the total amount of health research grant funds spent on this project for the entire duration of the grant, including indirect costs and any interest earned that was spent:

9(B) Provide the last names (include first initial if multiple individuals with the same last name are listed) of <u>all</u> persons who worked on this research project and were supported with health research funds. Include position titles (Principal Investigator, Graduate Assistant, Post-doctoral Fellow, etc.), percent of effort on project and total health research funds expended for the position. For multiple year projects, if percent of effort varied from year to year, report in the % of Effort column the effort by year 1, 2, 3, etc. of the project (x% Yr 1; z% Yr 2-3).

Last Name, First Name	Position Title	% of Effort on	Cost
		Project	
Ghazi, Arjumand	Principal Investigator	10.77% Yr 1,2,3	23,288.25
Gandhi Das, Francis	Post-Doctoral Fellow	100% Yr 1,2;50%	93,525.91
		Yr3	
Holden, Kyle	Research Technician	100% Yr 1,2;50%	57,438.66
		Yr3	

9(C) Provide the names of <u>all</u> persons who worked on this research project, but who *were not* supported with health research funds. Include position titles (Research Assistant, Administrative Assistant, etc.) and percent of effort on project. For multiple year projects, if percent of effort varied from year to year, report in the % of Effort column the effort by year 1, 2, 3, etc. of the project (x% Yr 1; z% Yr 2-3).

Last Name, First Name	Position Title	% of Effort on Project
Zoffel, Michael	Research Grants Admin.	5% Yrs 1-3
Ratnappan, Ramesh	Post-doctoral fellow	5% Year 2
Keith, Scott	Research Technician	5% Year 3
Sarah Winston	Summer student	100%; 1 summer Year 2
Martin Echavarria	Undergraduate student	50% for 1 semester Year 2
Sarah Bass	Summer student	50% for 1 summer Year 1
Hetal Patel	Undergraduate student	50% for 1 semester Year 2
Laura Smith	Master's rotation student	100% for 1 semester Year 2

9(D) Provide a list of <u>all</u> scientific equipment purchased as part of this research grant, a short description of the value (benefit) derived by the institution from this equipment, and the cost of the equipment.

Type of Scientific Equipment	Value Derived	Cost
21 cubic foot Freezer	Preserve sensitive samples and chemicals	699.95
4.5 cubic foot Refrigerator	Preserve sensitive samples and chemicals	199.95

10	. Co-funding of Research Project during Health Research Grant Award Period.	Did	this
	research project receive funding from any other source during the project period wh	en it v	was
	supported by the health research grant?		

Yes	No	X	

If yes, please indicate the source and amount of other funds:

# 11. Leveraging of Additional Funds

· / —		alth research funds provided for this research project, were you tain funding from other sources to continue or expand the
research?	ilid/Of Oc	and runding from other sources to continue of expand the
Yes	No	<u>X</u>

If yes, please list the applications submitted (column A), the funding agency (National Institutes of Health—NIH, or other source in column B), the month and year when the application was submitted (column C), and the amount of funds requested (column D). If you have received a notice that the grant will be funded, please indicate the amount of funds to be awarded (column E). If the grant was not funded, insert "not funded" in column E.

Do not include funding from your own institution or from CURE (tobacco settlement funds). Do not include grants submitted prior to the start date of the grant as shown in Question 2. If you list grants submitted within 1-6 months of the start date of this grant, add a statement below the table indicating how the data/results from this project were used to secure that grant.

A. Title of research	B. Funding	C. Month	D. Amount	E. Amount
project on grant	agency (check	and Year	of funds	of funds to
application	those that apply)	Submitted	requested:	be awarded:
	□NIH		\$	\$
	☐ Other federal			
	(specify:			
	□ Nonfederal			
	source (specify:			
	)			
	□NIH		\$	\$
	☐ Other federal			
	(specify:			
	)			
	☐ Nonfederal			
	source (specify:			
	)			
	□NIH		\$	\$
	☐ Other federal			
	(specify:			
	)			
	☐ Nonfederal			
	source (specify:			
	)			

11(B) Are yo the research?	11(B) Are you planning to apply for additional funding in the future to continue or expand the research?							
Yes <u>X</u>	Yes <u>X</u> No							
If yes, please	If yes, please describe your plans:							
mechanistic s	The aging-regulatory E3 ligases identified through this project will be the subject of mechanistic studies to understand the relationship between protein homeostasis, reproductive status and aging. We plan to submit a proposal of these experiments as an NIH grant.							
12. Future of Re	esearch Project. W	That are the future	e plans for this rese	earch project?				
needs to prote	ein homeostasis, qu	ality of aging and	l reproductive dem	nimal to balance the ands. The genes basis of these studies.				
	gator Training and ernships or graduat	_		ipate in project st one semester or one				
Yes <u>X</u>	No							
If yes, how m	nany students? Plea	ase specify in the	tables below:					
	Undergraduate	Masters	Pre-doc	Post-doc				
Male	4	1		2				
Female								
Unknown								
Total	4	1	0	2				
	TT 1 1 .	3.6	I D 1	I D . 1				

	Officergraduate	Masters	FIE-doc	rost-doc
Hispanic				
Non-Hispanic	3	1		2
Unknown	1			
Total	4	1	0	2

	Undergraduate	Masters	Pre-doc	Post-doc
White	3	1		
Black				
Asian				2
Other				
Unknown	1			
Total	4	1	0	2

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14.		t of Out-of-State research project?	Researchers. Did	you bring research	ers into Pennsylvania t	to
	Yes	NoX				
	If yes, please	list the name and	degree of each rese	earcher and his/her	previous affiliation:	
15.	-	- •	and Quality. Did		h project enhance the	
	Yes <u>X</u>	No				
	•	-	ents in infrastructure e and better researd		new investigators, and	
	setting up a resources inv studies has le	new laboratory, volved in the project to increased in	an undertaking thect. In addition, t	at would have be he preliminary da er faculty in areas	d exciting project whiten difficult without to ta generated from the such as proteomics an	he se
16.	Collaboratio	on, business and c	ommunity involve	ement.		
			unds lead to collab versity, entire hosp		ch partners outside of	
	Yes	No	<u>X</u>			
	If yes, ple	ease describe the c	ollaborations:			
	16(B) Did the	e research project	result in commercia	al development of	any research products?	
	Yes	No	X			

If yes, please describe commercial development activities that resulted from the research project:

16(C) Did the research lead to new involvement with the community?

Yes	No	X	

If yes, please describe involvement with community groups that resulted from the research project:

### 17. Progress in Achieving Research Goals, Objectives and Aims.

List the project goals, objectives and specific aims (as contained in the grant agreement). Summarize the progress made in achieving these goals, objectives and aims for the period that the project was funded (i.e., from project start date through end date). Indicate whether or not each goal/objective/aim was achieved; if something was not achieved, note the reasons why. Describe the methods used. If changes were made to the research goals/objectives/aims, methods, design or timeline since the original grant application was submitted, please describe the changes. Provide detailed results of the project. Include evidence of the data that was generated and analyzed, and provide tables, graphs, and figures of the data. List published abstracts, poster presentations and scientific meeting presentations at the end of the summary of progress; peer-reviewed publications should be listed under item 20.

This response should be a <u>DETAILED</u> report of the methods and findings. It is not sufficient to state that the work was completed. Insufficient information may result in an unfavorable performance review, which may jeopardize future funding. If research findings are pending publication you must still include enough detail for the expert peer reviewers to evaluate the progress during the course of the project.

Health research grants funded under the Tobacco Settlement Act will be evaluated via a performance review by an expert panel of researchers and clinicians who will assess project work using this Final Progress Report, all project Annual Reports and the project's strategic plan. After the final performance review of each project is complete, approximately 12-16 months after the end of the grant, this Final Progress Report, as well as the Final Performance Review Report containing the comments of the expert review panel, and the grantee's written response to the Final Performance Review Report, will be posted on the CURE Web site.

There is no limit to the length of your response. Responses must be single-spaced below, no smaller than 12-point type. If you cut and paste text from a publication, be sure symbols print properly, e.g., the Greek symbol for alpha  $(\alpha)$  and beta  $(\beta)$  should not print as boxes  $(\Box)$  and include the appropriate citation(s). DO NOT DELETE THESE INSTRUCTIONS.

### Regulation of Aging by the Proteasomal Pathway

This project attempts to understand how the reproductive status of an animal alters its rate of aging by modulating protein homeostasis mechanisms, especially the proteasomal pathway of protein ubiquitination. The main focus has been the identification of E3 ligase enzymes that change the rate of aging of an animal in response to signals from reproductive tissues. The nematode, C. elegans, is an ideal model organism for this project since it is particularly accessible to unraveling the relationship between reproduction and aging as well as protein homeostasis mechanisms. In worms, removal of germ cells increases lifespan by ~60% (1). The lifespan extension is not just a consequence of sterility; animals can be rendered sterile by multiple interventions but only when a pool of totipotent germline-stem cells (GSCs) is removed is its lifespan enhanced (2). This longevity is precisely regulated by, and dependent upon, the presence of a group of transcription factors. Two key transcription factors of this network include DAF-16, a conserved longevity determinant, and TCER-1, a transcriptionelongation factor that our previous studies found to specifically promote life in response to germline loss (1, 3). Previously, we had discovered that the proteasomal pathway of protein degradation regulates the aging of *C.elegans* (4). Specifically, we had found that inactivation of the CUL-1/SKR-1,-2/F-Box E3 ligase complex abolishes the extended lifespan of mutants of the insulin/IGF-1 receptor daf-2, that also rely on DAF-16 for their longevity. Our data suggested that the targeted proteasomal modification of specific substrate proteins is crucial for the extension of lifespan in C. elegans, by mutations in the daf-2 pathway (4). In this study, we attempted to identify proteasomal E3 ligases that mediate the longevity brought about by germline loss by employing large-scale RNAi screening. In addition to developing the RNAi screen, we planned to perform detailed secondary assays on the candidates obtained from the screen to identify bonafide lifespan-regulatory E3 ligases. Once identified, the E3 ligases could be used to discover the substrates whose proteasomal modification controls the long lifespan of germline-ablated worms. Following is a brief description of the progress achieved towards this end.

Specific Aim 1: To identify E3 ligases essential for lifespan extension brought about by germline removal

Aim 1 was partially achieved as reagents required for the E3-ligase screen were generated and the experimental set-up was standardized. Following are brief descriptions of the steps involved in this process.

i) Developing a Fluorescence-based Screening Strategy to Replace Longevity Read-out
To identify E3 ligase genes essential for lifespan extension mediated by germline loss, we
proposed to undertake an RNAi screen, using mutants for a gene called glp-1. The glp-1 gene
product is required for germ-cell proliferation; temperature sensitive glp-1 mutants lack germ
cells (at non-permissive temperature), are sterile, long-lived and have proven to be a valuable
surrogate for longevity produced by germline removal (2, 3). We first confirmed that glp-1
mutants exhibited the lifespan extension attributed to them at the restrictive temperature in a
new laboratory setting (the Ghazi lab was set up at the beginning of this project) and under
dependence of daf-16 and tcer-1. Based on the experience with the lifespan assays, we
revised our strategy to reduce the time of the screen (glp-1 mutants have a mean lifespan of
~28 days). We explored multiple options for designing a screen strategy in which the

molecular landmarks could be used as surrogates for longevity, including using transgenic worm strains carrying GFP-tagged DAF-16, TCER-1 as well as GFP expressed under control of their targets. Upon germline loss, DAF-16 becomes nuclear localized (5), TCER-1 levels rise transcriptionally (3) and the expression of both their targets is induced in intestinal cells (5, 6). Previously we had identified several genes that are up-regulated under control of DAF-16 and TCER-1 following germline ablation (3). These genes were studied using transgenic worm strains expressing GFP-tagged transcriptional fusion constructs that reported on the expression pattern of specific genes. Many of these genes exhibited striking increases in GFP levels in long-lived, glp-1 mutants, especially on Day 2 of adulthood (this reduced the screen time from ~30 to ~4 days). We considered using a reporter construct for one such gene, stdh-1, a common target of daf-16 and tcer-1 that is induced in intestinal cells of glp-1 mutants and is easily visible under the magnification provided by a stereomicroscope (3). However, we found that both DAF-16::GFP and TCER-1::GFP strains were not conducive for large-scale RNAi screens for independent reasons. TCER-1::GFP transgene is expressed at low levels that can only be observed under a compound microscope. Similarly, DAF-16::GFP nuclear localization was found to be variable and extremely sensitive to mild environmental perturbations. In addition, *Pstdh-1::GFP* was found to be regulated by multiple up-stream regulators, which made it as a non-specific reporter. However, in an independent project, in which we used Pstdh-1::GFP to screen a library of RNAi clones targeting worm nuclear hormone receptors (NHRs), we discovered a gene, nhr-49, that provided us with an ideal transgenic strain to screen for E3 ligases that mediate the reproductive control of aging.

### Generation of Transgenic Strain for RNAi Screen

We found that NHR-49, the worm functional homolog of human PPAR $\alpha$  proteins (7) is essential for the longevity of germline-less worms (Ratnappan et al., manuscript in preparation). NHR-49, similar to PPARα proteins, is an extremely important regulator of energy and fat metabolism (7) and its involvement in the germline-mediated control of aging raises interesting questions about the relationship between reproduction, fat and aging. As a part of the study that addressed the role of NHR-49 in regulating lifespan, we generated transgenic worms that express a GFP-tagged NHR-49 protein driven by its endogenous promoter (NHR-49::GFP). This construct was expressed in all somatic tissues of the worm in larval and adult stages and the levels of GFP rose when the animal lost its germline (Fig. 1). This strain expressed GFP at significantly higher levels than DAF-16::GFP or TCER-1::GFP strains and the fluorescence was clearly and widely visible under a stereo-microscope with a fluorescence attachment. In preliminary assays, we found that the transcriptional increase in expression of NHR-49 in germline-ablated worms is dependent on DAF-16 and TCER-1 (Fig. 1). This not only revealed to us the genetic pathway in which NHR-49 operates to mediate longevity, it also allowed us to standardize the conditions and timing under which NHR-49::GFP can be observed clearly.

### Genomic Integration of NHR-49::GFP Construct for RNAi Screen

In the original transgenic worms, the NHR-49::GFP construct was not integrated in the worm genome permanently (but carried as an extra-chromosomal array made up of concatemers of the DNA-construct that can be lost during cell divisions) and this resulted in two issues:

- (a) Heterogeneity of expression levels: since the number of DNA arrays could not be controlled within different cells, tissues and animals, there was a wide variation in the levels of GFP. As a result, the effects of any RNAi gene-inactivation on GFP levels was difficult to distinguish from the normal variation exhibited by a population unless very large numbers of worms were used.
- (b) Transgene transmission frequency: the extragenic nature of the array results in only a fraction of progeny of any transgenic worm carrying the GFP construct. Consequently, the strain needs to be maintained by manually picking fluorescent worms in each generation. Although our NHR-49::GFP transgenic strain showed a high-frequency of transmission (>80%), we found that for the purpose of an undertaking as a screen, it was arduous to work with an un-integrated strain.

To circumvent the above two issues, we integrated the NHR-49::GFP construct into the genome. This was performed using a standard technique that relies on the use of UV or  $\gamma$  rays to irradiate the parents. The radiation introduces DNA breaks that can undergo recombination with the extragenic array to cause integration of the transgene at relatively random genomic locations, usually in single copies. We used both UV and  $\gamma$  radiation (independently) for our experiment. Irradiated parents were allowed to lay eggs and their GFP+ve progeny were picked onto individual plates. In the next generation, about 600 lines were set up from the progeny of these fluorescent worms and scored for plates where all the worms were green. We isolated a single integrant from screening 600+ lines. The integrant was outcrossed six times to the lab wild-type stock (to eliminate background mutations that may have arisen from the radiation) and tested for authenticity of the NHR-49::GFP construct by RNAi tests.

### ii) RNAi Screen Paradigm on 24-well Petri dishes

While the integration of the NHR-49::GFP was in progress, we focused on developing a screen pipeline in which 24-well tissue-culture petri-dishes can be used to culture worms instead of regular 6cm nematode plates. This reduces the space and material requirements of the experiment and makes it possible to test much larger number of RNAi clones in a shorter duration. We determined that about 20-25 worms could be grown per well of a 24-well plate for 3-4 days without causing starvation or hypoxia or cross-contamination between wells. The increase in NHR-49::GFP upon loss of germline was found to be most striking on Day 2 of adulthood (~4 days of nematode culture) and this will be used as the major time-point for the screen. We are now conducting additional pilot tests (with RNAi sub-libraries targeting chromatin factors) to further fine-tune the screen conditions.

### iii) An Updated Proteasomal E3 Ligase RNAi Sublibrary

Our lab has a repository of two genome-scale feeding RNAi libraries that cover >87% of the worm genome (The Ahringer Library and the Vidal Library) (8, 9), and the E3 ligase RNAi clones to be used in the screen will be derived from these. We had previously generated an RNAi 'sub-library' targeting proteasomal genes. However, in the last two years the gene annotations for many genes have changed (<a href="www.wormbase.org">www.wormbase.org</a>) and this has resulted in the necessity for a new, updated 'sub-library'. We are now up-dating the virtual RNAi library to reflect the latest gene annotations. Once the sub-library is updated and re-constructed, we will perform the RNAi screen to identify E3 ligases that influence NHR-49 expression, and through this and other functional assays discover E3 ligases critical for longevity of

germline-ablated worms.

# iv) Developing secondary tests to identify bonafide lifespan-regulatory E3 ligases Since protein homeostasis is such a fundamental aspect of survival, reduced function of most proteasomal genes is highly deleterious to animal health and causes death rapidly. Consequently, it is difficult to distinguish the direct longevity functions of proteasome genes as compared to their role in cellular maintenance. One means of addressing this issue is to perform RNAi-inactivation of genes only in adult animals after the genes have fulfilled vital developmental functions (4). We have developed an RNAi strategy (Adult Only RNAi) to facilitate this, but by itself it is not sufficient. We have focused on this issue extensively, as tests that will help us identify E3 ligases whose RNAi-knockdown accelerates aging (as compared to treatments that just cause sickness and general dysfunction) will be the most crucial aspect of this project. In addition to testing the positive clones obtained from the screen for their effect on the extended lifespan of glp-1 mutants (by Adult Only RNAi), a series of morphometric assays, healthspan and stress-response tests can be used that reflect the overall health of the animal. Worms display characteristic age-related physical and functional deteriorations that are highly similar to features of human age-related decline, and can be quantified precisely (10, 11). Similarly, healthspan tests can be used to assess the rate of physiological aging. In addition, reduced resistance to environmental threats is a common feature of aging that is manifested in easily assayable manners in worms (12). Through exploratory pilot tests, we have finalized a series of healthspan tests that will evaluate the morphological and functional parameters of aging as well as stress-resilience of worms to give a comprehensive picture of the rate of aging of a population. RNAi clones identified from the screen that also reduce glp-1 longevity will be tested for their effects on the healthspan parameters. Clones that negatively impact these measures of overall health will be the most attractive candidates that will be studied molecularly. The healthspan assays are listed here in brief.

- 1. Morphometric Age-Associated Changes: Worms exhibit a series of well-characterized morphological changes that reflect the aging of tissues, similar to humans (10, 11). RNAi clones that influence NHR-49::GFP will be evaluated for their effect on the rate of aging by examining the anatomic age-related declines.
- (a) Sarcopenia: The deterioration undergone by muscle cells and nuclear architecture is easily evaluated using Nomarski optics (10, 11) and a population will be tested on Days 2, 3, 5 and 7 of adulthood.
- (b) Aging pigment accumulation: Lipofuscin and Advanced Glycation End products (AGEs) together constitute the age-related increase in intestinal autofluorescence (10, 11). We observe the accumulation of aging pigment fluorescence under a fluorescence microscope by using the DAPI filter (Ex/Em: 340nm/430nm) on Days 2, 3, 5 and 7. As a control, we also acquire the spectra at Ex/Em: 290nm/330nm to detect the signal generated by aromatic amino acids that does not change with age
- 2. Functional Age-related impairment: Similar to humans and other animals, aging nematodes also experience declining functionality (10). We have found that the following measures of functionality are easy and reliable markers that can be used on our screen candidates.

- (a) Loss of mobility: Closely associated with sarcopenia, reduced mobility can be directly correlated with the rate of aging, independent of the effect of a gene on length of life (10). We perform a chemo-attractant mobility assays on a population in which a group of agematched worms are placed at the center of a culture plate, and the average time taken by the animals to reach a drop of chemoattractant placed at one end of the plate is calculated. (b) Pharyngeal Pumping: Worms use a muscular pharynx to grind the bacteria they consume before it is transferred to the digestive tract. The rate of pumping undergoes a sharp decline with age (11). The pharynx is often compared to the human heart due to its muscle physiology, so this is a particularly useful assay to screen E3 ligases that influence aging. This test involves counting the number of pharyngeal pumps in a given interval of time (1min) for different members of a strain and comparing the averages between strains.
- 3. Decline in stress-tolerance: Longevity and stress-resistance are intimately related (12). Indeed, a large majority of long-lived mutants of various species are found to exhibit increased resistance to environmental stressors, including elevated temperatures, pathogens and atmospheric toxins (13). Alternatively, progeric mutants are extraordinarily sensitive to these threats (10, 11). Long-lived *glp-1* mutants are highly resistant to many stressors as compared to their normal, fertile counterparts (14). We have developed a compendium of stress assays that examine the resistance of a population to both biotic (pathogens) and abiotic (heat, oxidative stress etc.,), (Table 1) and RNAi clones identified from the screen will be evaluated for their effects on these paradigms.

#### Abiotic Stress Tests:

- (a) Osmotic Stress Test: We test for tolerance towards osmotic shock by exposing worms to high salt (500mM NaCl) and scoring for animals that loose motility over a period of 15 minutes. The same animals are then observed for an extended period of 12 hours to score for animals that are able to recover from the osmotic shock and regain motility. In addition, we also run a lifespan on these high salt plates for 72hrs till all the control wild-type animals die. We find that glp-1 mutants demonstrate greater resistance in each of these paradigms as compared to wild-type worms.
- (b) Oxidative Stress Test: Worms are exposed to concentrations of tert-Butyl Hydroperoxide (t-BOOH) and Paraquat, known inducer of oxidative stress, that are highly toxic to normal worms. *glp-1* mutants are able to survive these treatments for significantly longer periods than wild-type worms.
- (c) Heat Stress Test: We test for tolerance towards heat stress by exposing worms to high temperatures (35°C) and documenting the length of survival time. glp-1 mutants are highly resistant to heat stress as well.

### Biotic Stress Test:

Pathogen Stress Test: To test for immune resistance in glp-1 worms, we conduct a lifespan assay by transferring worms onto plates with pathogenic bacteria (Pseudomonas aeruginosa). glp-1 survive longer periods on two pathogenic strains, PA14 and PA01, as compared to fertile worms.

### *Uncoupling (Oxidative) Stress Resistance from Lifespan:*

In standardizing the stress assays described above, we made some startling discoveries.

Resistance to a variety of stressors such as oxidative agents, high temperature, pathogens and heavy metals, is found to be highly correlated with long life. Most long-lived mutants demonstrate extraordinary resilience towards one or more of these stressors (13). Our previous studies and those of others (14) had shown that this is true of GSC-ablated worms as well. We tested daf-16 and tcer-1 RNAi clones as positive controls in these stress experiments, since daf-16 has previously been shown to underlie a majority of the worms' stress-resistance. However, we were surprised to observe that tcer-1 RNAi did not abrogate the resistance of germline-ablated worms to an oxidative stress-inducing agent, t-Butyl Hydroperoxide (t-BOOH), while daf-16 RNAi did (Amrit FG and Ghazi A, unpublished data). We found this to be particularly true for oxidative stress. This data is interesting as it suggests that there may be proteins (such as DAF-16) that confer both longevity and stressresistance, whereas there may be other proteins that specifically alter the length of life, without any effect on stress-resistance (such as TCER-1). These implications could extend to the E3-ligases we are studying. Specifically, our healthspan assays will help us distinguish E3 ligases that influence longevity specifically, without altering stress-resistance, from those that simultaneously promote longevity and stress resistance. Of the latter class, it will be informative to identify E3 ligases that confer broad resistance to many stressors as well as those that are specific to individual stress paradigms.

Specific Aim 2: To identify substrates of E3 ligases whose controlled degradation is required for the extended lifespan of *glp-1* mutants
Aim 2 was partially achieved. The transcription factor, SKN-1/NRF2, was identified as a potential target of LIN-23/bTRCP, The details are described below.

Specific Aim 3: To perform detailed cellular and molecular analyses of identified substrates Aim 3 was partially achieved. We examined the role of SKN-1/NRF2 in mediating lifespan extension as well as stress-resistance in worms and analyzed the genetic circuit in which it functions to mediate these functions.

# <u>The LIN-23/βTRCP and SKN-1/NRF2 Pathway in Regulating Reproductive Control of Aging:</u>

In previous experiments, we had identified an F-Box adaptor protein LIN-23 as one of the E3-ligase components essential for the longevity of insulin/IGF-1 receptor, daf-2, mutants (4). LIN-23 is the worm homolog of a highly conserved E3-ligase protein in mammals,  $\beta$ TRCP. Both LIN-23 and  $\beta$ TRCP have been shown to function in the CUL-1/SKR-1/2 E3-ligase complex in worms and humans, respectively (15). In addition,  $\beta$ TRCP is also a key regulator of the human NRF2 transcription factor whose worm homolog is SKN-1 (16). We have explored this relationship between the worm LIN-23/ $\beta$ TRCP and SKN-1/NRF2 proteins. SKN-1, the worm homolog of NRF2 is a key transcription factor that promotes longevity and stress-resistance. We found that it is part of the transcriptional circuit that gets activated upon germline loss in intestinal cells, and is required for the longevity of glp-1 mutants. We also discovered that LIN-23/ $\beta$ TRCP is essential for the up-regulation of SKN-1/NRF2 target genes that mitigate oxidative stress, and for the enhanced stress-resistance of long-lived worms (Fig. 2). We confirmed that SKN-1/NRF2 becomes nuclear localized following germ-cell loss and are exploring the relationship between the E3 ligase (LIN-23) and its substrate (SKN-1) that influence the reproductive control of aging.

### References

- 1. Hsin H, Kenyon C. Signals from the reproductive system regulate the lifespan of *C. elegans. Nature.* 1999. 399(6734):362-6.
- 2. Arantes-Oliveira N, Apfeld J, Dillin A, Kenyon C. Regulation of life-span by germ-line stem cells in *Caenorhabditis elegans*. *Science*. 2002. 295(5554):502-5.
- 3. Ghazi A, Henis-Korenblit S and Kenyon C. A transcription elongation factor that links signals from the reproductive system to lifespan extension in *Caenorhabditis elegans* (2009).*PLoS Genetics*. 2009. 5(9):e1000639.
- 4. Ghazi A, Henis-Korenblit S, Kenyon C. Regulation of *Caenorhabditis elegans* lifespan by a proteasomal E3 ligase complex. *Proceedings of the National Academy of Sciences of the United States of America*. 2007. 104(14): 5947-52.
- 5. Lin K, Hsin H, Libina N, Kenyon C. Regulation of the *Caenorhabditis elegans* longevity protein DAF-16 by insulin/IGF-1 and germline signaling. *Nat Genet.* 2001. 28(2):139-45.
- 6. Libina N, Berman JR and Kenyon C. Tissue-specific activities of *C. elegans* DAF-16 in the regulation of lifespan. *Cell.* 2003. 115: 489-502.
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- 15. Kipreos ET, Gohel SP, Hedgecock EM. The C. elegans F-box/WD-repeat protein LIN-23 functions to limit cell division during development. Development. 2000 Dec;127(23):5071-82.

16. Tullet JM, Hertweck M, An JH, Baker J, Hwang JY, Liu S, Oliveira RP, Baumeister R, Blackwell TK. Direct inhibition of the longevity-promoting factor SKN-1 by insulin-like signaling in C. elegans. Cell. 2008 Mar 21;132(6):1025-38. doi: 10.1016/j.cell.2008.01.030.

# Figures and Table

Figure 1

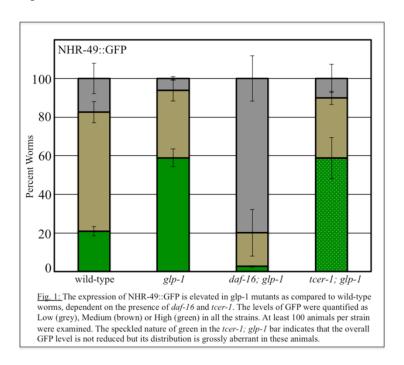


Table 1: Stress assays to examine the effect of E3-ligases gene inactivation on the healthspan and rate of aging of a population

Stress Type	Stress Agent	Experimental Conditions	Average Lifespan of wild-type worms
Oxidative	Paraquat	7mM continuous exposure	4-6hrs
Stress	t-BOOH	6.2mM for 1hr	4–8hrs
Thermal Stress	Heat	35°C for 2hrs	7-9hrs
Osmotic Stress	Sodium Chloride	500-700mM	18-24hrs
Pathogenic Bacteria	P. aeruginosa PA14 PA01	Young adults transferred to pathogen plates and examined at regular intervals (15min for PA01 and 3hrs for PA14)	PA14: 3-4 days PA01: 4 hours

Figure 2

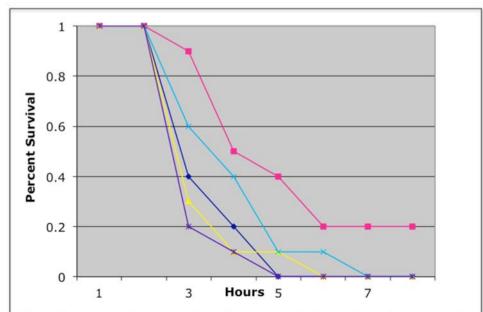


Fig. 2: The E3-ligase LIN-23/bTRCP and its substrate SKN-1/NRF2 are both essential for the oxidative stress resistance of long-lived mutants. Survival of Day 2 young adults exposed to 7mM Paraquat was compared between wild-type worms (blue) and *daf-2* mutants grown on empty vector (RNAi control pink), *lin-23* RNAi (yellow), *skn-1* RNAi (light blue) and *daf-16* RNAi (purple). Control *vs. lin-23* RNAi, p<0.01; Control *vs skn-1* RNAi p<0.05; Control *vs daf-16* RNAi p<0.001; wild-type *vs daf-2* control p<0.01

### Meeting Abstracts:

1. Kyle Holden<sup>\$</sup>, Emmanuel Schrieber, Mani Balasubramani and Arjumand Ghazi\*. The E3 Ligase LIN-23/βTRCP Influences SKN-1/NRF2 Activity and Reduces Toxic Proteins in *daf-2* Mutants.

Department of Pediatrics, Rangos Research Centre, University of Pittsburgh School of Medicine. \$Presenting Author; \*Corresponding Author: Arjumand.Ghazi@chp.edu Presented at 19<sup>th</sup> *International C. elegans Meeting*. University of California, Los Angeles, June 2013.

2. Kyle Holden<sup>\$</sup>, Emmanuel Schrieber, Mani Balasubramani and Arjumand Ghazi\*. The E3 Ligase LIN-23/ $\beta$ TRCP Influences SKN-1/NRF2 Activity and Reduces Toxic Proteins in *daf-2* Mutants.

Department of Pediatrics, Rangos Research Centre, University of Pittsburgh School of Medicine. \$Presenting Author; \*Corresponding Author: Arjumand.Ghazi@chp.edu Presented at Annual Aging Day of the Aging Institute of University of Pittsburgh. 2013.

3. Kyle Holden<sup>\$</sup> and Arjumand Ghazi\*. Identification of substrates of E3 ligases that promote longevity

Department of Pediatrics, Rangos Research Centre, University of Pittsburgh School of Medicine. \$\frac{1}{2}Presenting Author; \*Corresponding Author: Arjumand.Ghazi@chp.edu Presented at Rangos Research Day of the Rangos Research Center, Children's Hospital of Pittsburgh. 2013

4. Sarah Winston<sup>\$</sup>, Francis A. Gandhi and Arjumand Ghazi\*. The Regulation of Stress-Response Pathways by the Germline in *C. elegans*Department of Pediatrics, Rangos Research Centre, University of Pittsburgh School of Medicine. <sup>\$</sup>Presenting Author; \*Corresponding Author: Arjumand.Ghazi@chp.edu
Presented at Summer Student Research Presentation. Children's Hospital of Pittsburgh, July 2012.

**18. Extent of Clinical Activities Initiated and Completed**. Items 18(A) and 18(B) should be completed for all research projects. If the project was restricted to secondary analysis of clinical data or data analysis of clinical research, then responses to 18(A) and 18(B) should be "No."

18(A) Did you initiate a study that involved the testing of treatment, prevention or

diagnostic pr	ocedures on human subjects?
Y	es
XN	No
18(B) Did yo	ou complete a study that involved the testing of treatment, prevention or
diagnostic pr	ocedures on human subjects?
Y	
XN	No.
complete 18(C-F) if	<b>8(A)</b> or <b>18(B)</b> , items <b>18(C)</b> – ( <b>F</b> ) must also be completed. (Do NOT 18(A) and 18(B) are both "No.")  many hospital and health care professionals were involved in the research
project?	
	fumber of hospital and health care professionals involved in the research roject
18(D) How r	many subjects were included in the study compared to targeted goals?
	Sumber of subjects originally targeted to be included in the study sumber of subjects enrolled in the study
<u>Note</u> : Stu	idies that fall dramatically short on recruitment are encouraged to

provide the details of their recruitment efforts in Item 17, Progress in Achieving Research Goals, Objectives and Aims. For example, the number of eligible subjects approached, the number that refused to participate and the reasons for

refusal. Without this information it is difficult to discern whether eligibility criteria were too restrictive or the study simply did not appeal to subjects.

18(E) How many subjects were enrolled in the study by gender, ethnicity and race?

Gender:
Males
Females
Unknown
Ethnicity:
Latinos or Hispanics
Not Latinos or Hispanics
Unknown
Race:
American Indian or Alaska Native
Asian
Blacks or African American
Native Hawaiian or Other Pacific Islander
White
Other, specify:
Unknown
18(F) Where was the research study conducted? (List the county where the research study was conducted. If the treatment, prevention and diagnostic tests were offered i more than one county, list all of the counties where the research study was conducted.)
<b>Human Embryonic Stem Cell Research.</b> Item 19(A) should be completed for all research projects. If the research project involved human embryonic stem cells, items 19(B) and 19(C) must also be completed.
19(A) Did this project involve, in any capacity, human embryonic stem cells? Yes
19(B) Were these stem cell lines NIH-approved lines that were derived outside of
Pennsylvania?
Yes
No
19(C) Please describe how this project involved human embryonic stem cells:

19. Human

in

### 20. Articles Submitted to Peer-Reviewed Publications.

20(A) Identify all publications that resulted from the research performed during the funding period and that have been submitted to peer-reviewed publications. Do not list journal abstracts or presentations at professional meetings; abstract and meeting presentations should be listed at the end of item 17. **Include only those publications that acknowledge the Pennsylvania Department of Health as a funding source** (as required in the grant agreement). List the title of the journal article, the authors, the name of the peer-reviewed publication, the month and year when it was submitted, and the status of publication (submitted for publication, accepted for publication or published.). Submit an electronic copy of each publication or paper submitted for publication, listed in the table, in a PDF version 5.0.5 (or greater) format, 1,200 dpi. Filenames for each publication should include the number of the research project, the last name of the PI, and an abbreviated title of the publication. For example, if you submit two publications for Smith (PI for Project 01), one publication for Zhang (PI for Project 03), and one publication for Bates (PI for Project 04), the filenames would be:

Project 01 – Smith – Three cases of isolated

Project 01 – Smith – Investigation of NEB1 deletions

Project 03 – Zhang – Molecular profiling of aromatase

Project 04 – Bates – Neonatal intensive care

If the publication is not available electronically, provide 5 paper copies of the publication.

<u>Note:</u> The grant agreement requires that recipients acknowledge the Pennsylvania Department of Health funding in all publications. Please ensure that all publications listed acknowledge the Department of Health funding. If a publication does not acknowledge the funding from the Commonwealth, do not list the publication.

Title of Journal	Authors:	Name of Peer-	Month and	Publication
Article:		reviewed	Year	Status (check
		Publication:	Submitted:	appropriate box
				below):
1. The C. elegans	Scott Alexander	Methods	February	Published
Healthspan and	Keith, Francis Raj		2014	
Stress-Response	Gandhi Amrit,			
Assay Toolkit	Ramesh Ratnappan			
	and Arjumand			
	Ghazi			
2. The <i>C. elegans</i>	Francis Raj Gandhi	Methods	February	Published
Lifespan Assay	Amrit, Ramesh		2014	
Toolkit	Ratnappan, Scott			
	Alexander Keith,			
	and Arjumand			
	Ghazi			

	Based o future?	n this project, are you planning to submit articles to peer-reviewed publications
		Nolescribe your plans:
LIN-23/β' addresses experimen	TRCP ar the unco nts are co	ascript in preparation that addresses the relationship between the E3-ligase and its substrate SKN-1/NRF2 in the context of aging. A second manuscript that oupling of stress-resistance and aging will be written after additional oncluded. In addition, we plan to submit the screen proposed in this project as a completed.
Descri impac or othe there v single	ibe the o t on the er releva were no -spaced	utcome, Impact and Effectiveness Attributable to the Research Project. utcome, impact, and effectiveness of the research project by summarizing its incidence of disease, death from disease, stage of disease at time of diagnosis, int measures of outcome, impact or effectiveness of the research project. If changes, insert "None"; do not use "Not applicable." Responses must be below, and no smaller than 12-point type. DO NOT DELETE THESE WNS. There is no limit to the length of your response.
None		
Treat diagno no ma Respo	ment. Dosis and to jor disconnes mu	eries, New Drugs, and New Approaches for Prevention Diagnosis and Describe major discoveries, new drugs, and new approaches for prevention, treatment that are attributable to the completed research project. If there were everies, drugs or approaches, insert "None"; do not use "Not applicable." at be single-spaced below, and no smaller than 12-point type. DO NOT ESE INSTRUCTIONS. There is no limit to the length of your response.
None		
23. Inven	tions, Pa	atents and Commercial Development Opportunities.
of the	United S	by inventions, which may be patentable or otherwise protectable under Title 35 States Code, conceived or first actually reduced to practice in the performance this health research grant? Yes NoXX
		(A), complete items a – g below for each invention. (Do NOT complete items is "No.")
a.	Title of	Invention:
b.	Name o	of Inventor(s):
c.		cal Description of Invention (describe nature, purpose, operation and physical, al, biological or electrical characteristics of the invention):

d.	Was a patent filed for the invention conceived or first actually reduced to practice in the performance of work under this health research grant?
	Yes No
	If yes, indicate date patent was filed:
e.	Was a patent issued for the invention conceived or first actually reduced to practice in the performance of work under this health research grant?  Yes No  If yes, indicate number of patent, title and date issued:  Patent number:  Title of patent:  Date issued:
f.	Were any licenses granted for the patent obtained as a result of work performed under this health research grant? Yes No
	If yes, how many licenses were granted?
g.	Were any commercial development activities taken to develop the invention into a commercial product or service for manufacture or sale? Yes No
	If yes, describe the commercial development activities:
	Based on the results of this project, are you planning to file for any licenses or patents, lertake any commercial development opportunities in the future?
Yes	No <u>X</u>
If yes,	please describe your plans:
	<b>Tey Investigator Qualifications.</b> Briefly describe the education, research interests and ence and professional commitments of the Principal Investigator and all other key

investigators. In place of narrative you may insert the NIH biosketch form here; however, please limit each biosketch to 1-2 pages. For Nonformula grants only – include information for only those key investigators whose biosketches were not included in the original grant

application.

Biographical Sketch		
NAME GHAZI, ARJUMAND	POSITION TITLE Assistant Professor of Pediatrics,	
eRA COMMONS USER NAME ARJUMAND	of Developmental Biology and Cell Biology	

# EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	MM/YY	FIELD OF STUDY
St. Ann's College, Osmania University, Hyderabad, India	B.S.	06/93	Microbiology, Chemistry, Zoology
Hyderabad Central University, Hyderabad, India	M.S.	06/95	Biotechnology
National Centre for Biological Sciences (NCBS), Tata Institute for Fundamental Research (TIFR) Centre, Bangalore, India	Ph.D.	11/01	Developmental Biology, Genetics
University of California, San Francisco (UCSF)	Postdoc	06/02-05/07	Genetics of Aging

# Positions and Honors Positions and Employment

Positions and Employme	<u>ent</u>
Aug Dec. 1999	Visiting Fellow, Institut de Genetique et de Biologie Moleculaire et
Cellulaire	(IGBMC), Strasbourg, France
Apr. 2001-Apr. 2002	Visiting Fellow, National Centre of Biological Sciences (NCBS),
TIFR Centre,	Bangalore, India
June 2002-June 2007	Postdoctoral Scholar, University of California, San Francisco
(UCSF)	
July 2007- Jan. 2010	Associate Research Specialist, University of California, San
Francisco (UCSF)	
Dec. 2010	Visiting Professor, University of Pittsburgh School of Medicine
Jan 2011-present	Tenure Track Assistant Professor, University of Pittsburgh School of
Medicine	

Honors	
2013	Session Chair, 'Aging and Stress' Session, 19th International C. elegans Meeting
2012	Ellison Medical Foundation's New Scholars in Aging award
2012	American Heart Association Beginning Grant-in-Aid award (declined)
2012	Competitive Medical Research Fund (CMRF) award of the University of Pittsburgh
	(declined)
2012	Invited to submit application for Basil O'Connor award of March of Dimes foundation
	(declined)
2012	Session Chair, C. elegans meeting on 'Aging, Stress, Pathogenesis and small RNAs'
2011	Research Advisory Committee Children's Hospital of Pittsburgh New Investigator
	grant
2011	American Federation for Aging Research (AFAR) grant

2011	Kimble Chase New Lab Start-up grant
2011	University of Pittsburgh Clinical and Translational Science Institute Translational
	Technologies Cores Pilot Program
2010	Pennsylvania Department of Health, Health Research Formula Funds
2009	Publication recommended by Faculty of 1000 (Ghazi et al., 2009;
	http://www.f1000biology.com/article/id/1163908/evaluation)
2008	Best Poster Prize, 15 <sup>th</sup> International C. elegans Meeting, UCLA
2006	Larry L. Hillblom Foundation for Aging Postdoctoral Research Grant
2004	Indian National Science Academy (INSA) Young Scientist Award
2003	American Federation for Aging Research (AFAR) Postdoctoral fellowship
2002	Scientific Advisory Board Assistant, Science of Aging Knowledge Environment of the journal 'Science'
2002	Cold Spring Harbor Laboratory fellowship (to attend the course 'C. elegans')
2001	Best Poster Prize, International Cell and Developmental Biology Symposium,
	Bangalore, India
1999	Institute of Genetics and Molecular and Cell Biology (IGBMC) research support
1999	WoodWhelan Research Fellowship, International Union of Biochemists and Molecular Biologists
1999	Journal of Cell Science Fellowship, Company of Biologists
1998	Best Poster Prize, International Cell Cycle Meeting, Ullal, India
1998	Cold Spring Harbor Laboratory Fellowship (to attend 'Neurobiology of <i>Drosophila</i> ')
	(Declined)
1998	Surdna Foundation Scholarship, Marine Biological Laboratory (MBL), Woodshole
1995	Ranked 31 <sup>st</sup> (99.8 percentile) All India Graduate Aptitude Test in Engineering conducted by the Indian Institutes of Technology (IITs)
1995	Council for Scientific and Industrial Research (CSIR), India, Graduate Fellowship
	(Declined)
1994	Centre for Cellular and Molecular Biology (CCMB), India, Summer Research
	Fellowship
1993	Department of Biotechnology, India, Master's in Biotechnology Scholarship
1993	Valedictorian, St. Ann's College, Osmania University, Hyderabad, India

### **PUBLICATIONS**

- 1. **Ghazi A.** Transciptional networks that mediate signals from reproductive tissues to influence lifespan. *genesis*, **The Journal of Genetics and Development** doi: 10.1002/dvg.22345. 2013.
- 2. **Ghazi A,** Henis-Korenblit S, Kenyon C. A transcription elongation factor that links signals from the reproductive system to lifespan extension in *Caenorhabditis elegans*. *PLoS Genet* 5(9):e1000639, 2009. PMID: 19749979.
  - (Recommended by Faculty of 1000) <a href="https://www.f1000biology.com/article/id/1163908/evaluation">www.f1000biology.com/article/id/1163908/evaluation</a>
- 3. **Ghazi A\***, Henis-Korenblit S\*, Kenyon C. Regulation of *Caenorhabditis elegans* lifespan by a proteasomal E3 ligase complex. *Proc Natl Acad Sci USA* 104(14):5947-5952, 2007. PMID: 17392428 \*equal contribution
  - Focus of 'Dispatch' Article: Bruce Bowerman (2007). C. elegans Aging. Proteolysis cuts both ways. Current Biology (2007) 17(13): R514-16.
- 4. **Ghazi A**, Paul L, VijayRaghavan K. Prepattern genes and signaling molecules regulate stripe expression to specify *Drosophila* flight muscle attachment sites. *Mech Dev* 120(5):519-528, 2003. PMID: 12782269

- 5. **Ghazi A**, VijayRaghavan K. Muscle Development in *Drosophila*. *Proc Ind Natl Sci Acad* 5:691-702, 2003.
- 6. **Ghazi A**, Anant S, VijayRaghavan K. Apterous mediates development of direct flight muscles autonomously and indirect flight muscles through epidermal cues. *Development* 127(24):5309-5318, 2000. PMID: 11076753
- 7. **Ghazi A**, VijayRaghavan K. Developmental biology. Control by combinatorial codes. *Nature* 408(6811):419-420, 2000. PMID: 11100709 *Manuscripts under review*
- 8. Amrit FG, Ratnappan R, Keith SA and **Ghazi A.** The *C. elegans* Lifespan and Healthspan Toolkit. Invited review article for the journal *Methods*
- 9. Amrit FG, Ratnappan R, Keith SA and **Ghazi A.** The *C. elegans* Lifespan and Healthspan Toolkit. Invited review article for the journal *Methods*= *Additional publications relevant to the field*
- 10. **Ghazi A.** (2002). Puzzling over research on Aging. Crossword Puzzle on Aging Research. *SAGE KE, Perspectives*.
- 11. **Ghazi A** & Kenyon C. Cells of the somatic gonad that promote *C. elegans* longevity. Manuscript in preparation.

Manuscripts in preparation from work at the University of Pittsburgh

- Ratnappan R, Amrit FG, Ward J, Gill H, Holden K, Olsen CP, Yamamoto K and Ghazi
   A. Reproductive Signals Deploy NHR-49/PPARα to Enhance Fatty Acid β-Oxidation and Desaturation and Increase Lifespan
- 13. Amrit FG, McClendon B, Ratnappan R, Arora A, Benos T, Yanowitz J and **Ghazi A**. TCER-1/TCERG1 and DAF-16/FOXO Balance Fertility and Longevity in Response to Germline Signals by Controlling Genes Involved in Reproduction and Lipid Homeostasis
- 14. Holden K, Keith SA, Schreiber M, Balasubramani M and **Ghazi A**. Proteomic Analysis of LIN-23/βTRCP Reveals Novel Targets and that Influence Longevity and Stress-Resistance through Regulation of SKN-1/NRF2
- 15. Gill H, Amrit FG, Stolz DB and **Ghazi A**. Use of Scanning Electron Microscopy (SEM) to document age-related cuticular deterioration in *C. elegans*.
- 16. Ratnappan R, Amrit FG, Keith SA and **Ghazi A. Reproductive Regulation of Aging.** Invited review for the journal *Current Genetic Medical Reports*
- **C. Research Support** (ongoing, pending and completed projects)

### **Current:**

Ellison Medical Foundation, New Scholars in Aging award miRNAs and lipophilic-hormonal pathways that relay reproductive signals to control aging 7/1/2012-6/30/2016 \$400,000

This project explores the role of miRNAs and lipophilic-signaling genes in controlling longevity.

### **Completed:**

American Federation of Aging Research (AFAR), AFAR Research Grant Study of reproductive signals that regulate aging 7/1/2011-6/30/2013 \$100,000

This project focused on identification of new genes involved in the reproductive control of aging.

Children's Hospital of Pittsburgh, Research and Advisory Committee New Investigator grant Control of Longevity Genes by 'Paused' RNA Polymerase II and Regulated Transcript Elongation.

1/1/2012-12/31/2013 \$64,000

This project focused on the study of paused RNA polymerases in aging.

Pennsylvania Department of Health, Health Research Formula Funds

Regulation of aging by the proteasomal pathway

1/1/2011 - 12/31/2013 \$327,174 (part of start-up funds)

This project focused on proteasomal E3 ligases involved in reproductive control of aging.

University of Pittsburgh Clinical and Translational Science Institute, Translational Technologies Cores Pilot Program

Proteomic analysis of F-Box substrates that promote longevity

7/1/2011 - 6/30/2012 \$15,000 (core services)

This project used proteomics to identify E3-ligase substrates that regulate aging of *daf-2* mutants.

Larry L. Hillblom Foundation for Aging Research Grant, Regulation of aging by the proteasomal pathway of protein degradation

6/1/06-5/30/09 \$180,000

This project focused on the proteasomal regulation of lifespan.

American Federation of Aging Research Grant, Role of the somatic gonad in the regulation of *C. elegans* aging

7/1/2003-6/30/2005 \$50,000

This project aimed to identify cells of the somatic gonad that promote longevity in worms.